



1/9

PRIMER G →

```

1 aaacaagataaaacatgatttatcaacatTTTTactTTTccactttctgtggaa
1-----+-----+-----+-----+-----+-----+-----+-----+60

61 aactttattaaaatatccacttacccattatTTTTtagattatccacaaaaatgtgga
61-----+-----+-----+-----+-----+-----+-----+-----+120

121 gaaactataatttagttgatTTTgttactattaaggtattaagtgagagtagattata
121-----+-----+-----+-----+-----+-----+-----+-----+180

181 attacatcatagaatgctacaaagattaataattgaaaggaattatttatgcaaaagc
181-----+-----+-----+-----+-----+-----+-----+-----+-----+240
                                         RBS
                                         M A K A

241 taatataggaaaattgctattaacagggtgtcggtggcgagccatcgacttggaggaag
241-----+-----+-----+-----+-----+-----+-----+-----+-----+300
      N I G K L   L L T G V V G G A I A L G G S
      TRANSMEMBRANE DOMAINE

301 tgcaatctatcaaaggactacaaatcaatcgcaaataatagtcgttcaaataactag
301-----+-----+-----+-----+-----+-----+-----+-----+-----+360
      A I Y Q S T F N Q S A N N S R S N T T S
      T K V S N V S V N V N T D V T S A I E K

361 tacaaggtagtaacgTTTcgtaatgtcaataccgatgttacctctgcaattgaaaa
361-----+-----+-----+-----+-----+-----+-----+-----+-----+420
      T K V S N V S V N V N T D V T S A I E K

421 agttcaattctgtcgTTTctgttatgaattatcaaaaagataactcacaaagttagtga
421-----+-----+-----+-----+-----+-----+-----+-----+-----+480
      V S N S V V S V M N Y Q K D N S Q S S D
      F S S I F G G N S G S S S T D G L Q L

481 cttagttcaattttgggtggaaatagcggttcaagttcatcgactgatggcttacagct
481-----+-----+-----+-----+-----+-----+-----+-----+-----+540
      F S S I F G G N S G S S S T D G L Q L
      ttctagtgaaggctctgggtcatctacaaaaaatctgggtggatgcctacgttgtaac
541-----+-----+-----+-----+-----+-----+-----+-----+-----+600
      S S E G S G V I Y K K S G G D A Y V V T
      CATALYTIC DOMAINE

601 taactaccacgttattgctggtaatagctactgtatgttctgtttctgggacaaaaa
601-----+-----+-----+-----+-----+-----+-----+-----+-----+660
      N Y H V I A G N S S L D V L L S G G Q K
  
```

FIG. 1

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661 agtcaaagattctgtggggttatgtatgaatacacacagacccgtgtttaaaatcag
 661-----+-----+-----+-----+-----+-----+-----+-----+
 V K D S V V G Y D E Y T **D L A V L K I S**
 CATALYTIC DOMAINE
 721 ttctgaacatgtcaaagatgtggcgacattcgctgattcttagtaaaattaacaatttgtga
 721-----+-----+-----+-----+-----+-----+-----+-----+
 S E H V K D V A T F A D S S K L T I G E
 781 acctgccattgccgttggctcaccttaggttagtcaatttgcaaacaccgcaactgaagg
 781-----+-----+-----+-----+-----+-----+-----+-----+
 P A I A V G S P L G S Q F A N T A T E G
 841 aattttatctgcaacaaggccgtcaagtgactttgacccaagaaaaatggtcaaacaactaa
 841-----+-----+-----+-----+-----+-----+-----+-----+
 I L S A T S R Q V T L T Q E N G Q T T N
 ← PRIMER A
 901 tatcaatgcaattcaaacagatgctgccatttaaccctggtaactctggaggggcttgat
 901-----+-----+-----+-----+-----+-----+-----+-----+
 I N A I Q T D A A I N P **G N S G G A L I**
 CATALYTIC DOMAINE
 961 taatattgaaggacaagttattgaaattactcaaagtaaaattacaacaactgaagatgg
 961-----+-----+-----+-----+-----+-----+-----+-----+
N I E G Q V I G I T Q S K I T T T E D G
 1021 ttctacttctgtcgaagggtttaggattgcgattccttcaatgatgtcgtaaatatcat
 1021-----+-----+-----+-----+-----+-----+-----+-----+
 S T S V E G L G F A I P S N D V V N I I
 1081 taataaactgaagatgatgtaagatttcacgcctgcttaggtatccgaatggta
 1081-----+-----+-----+-----+-----+-----+-----+-----+
 N K L E D D G K I S R P A L G I R M V D
 1141 ccttcacaattatcaacaaatgacagttctcaattgaaattactaaggcagtgtacagg
 1141-----+-----+-----+-----+-----+-----+-----+-----+
 L S Q L S T N D S S Q L K L L S S V T G
 1201 tgggttgttactccgtccatctggacttcctgctgcctcagctggttgaaagc
 1201-----+-----+-----+-----+-----+-----+-----+-----+
 G V V V Y S V Q S G L P A A S A G L K A
 1261 tggagatgtaattacaaagggttggcgatacagcagtaacaccttcaacagacttgcaaag
 1261-----+-----+-----+-----+-----+-----+-----+-----+
 G D V I T K V G D T A V T S S T D L Q S

FIG. 1
(CONTINUED)

tgctcttactcacacaatcaatgatacagtaaaagttaacttattatcgatggtaa
1321-----+-----+-----+-----+-----+-----+-----+-----+-----+1380
A L Y S H N I N D T V K V T Y Y R D G K

atcaaatacagcagatgttaactttctaaatcaaccagtgacttagaaacaaggcgtcc
1381-----+-----+-----+-----+-----+-----+-----+-----+-----+1440
S N T A D V K L S K S T S D L E T S S P

atcttcttctaatt**a**taacttaataatttaataaaaagtcttctgttaatagaaggctt
1441-----+-----+-----+-----+-----+-----+-----+-----+1500
S S S N

tttcataactaaagtctgaaattttaaaaataataaaattccattttctttattgatt
1501-----+-----+-----+-----+-----+-----+-----+-----+1560

tatggtaaaataaagttaagcatgaaaatttactttacttagaagccgaacaattttg
1561-----+-----+-----+-----+-----+-----+-----+-----+1620

agtcattcaggaattggtcgtgcaatgaaacatcaacaacgcgcgccttgatttaatggc
1621-----+-----+-----+-----+-----+-----+-----+-----+1680

attgactggacaaaaaatcctgaggatgattacgatattccattaaatacttatggc
1681-----+-----+-----+-----+-----+-----+-----+-----+1740

FIG. 1
(CONTINUED)

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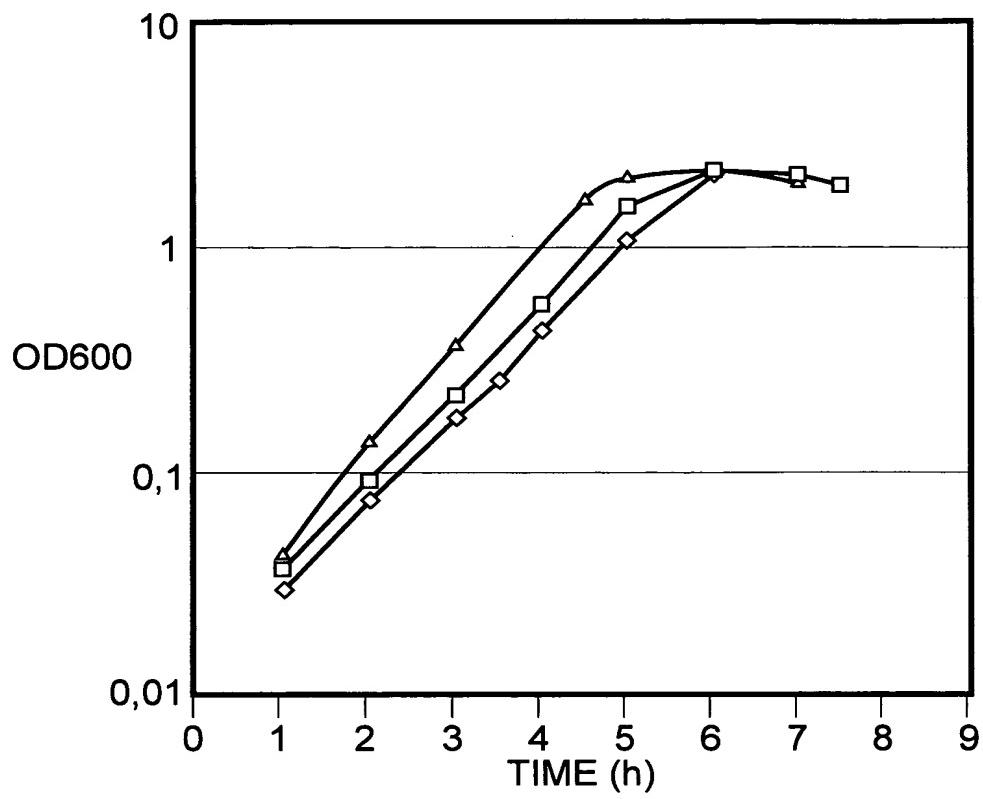


FIG. 2A

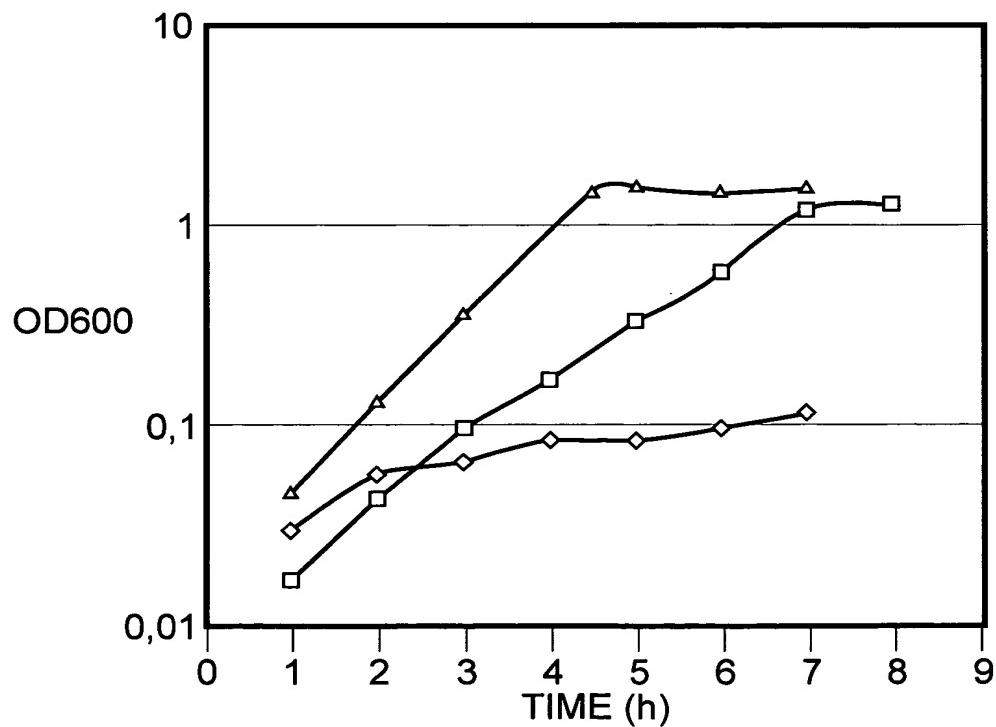


FIG. 2B

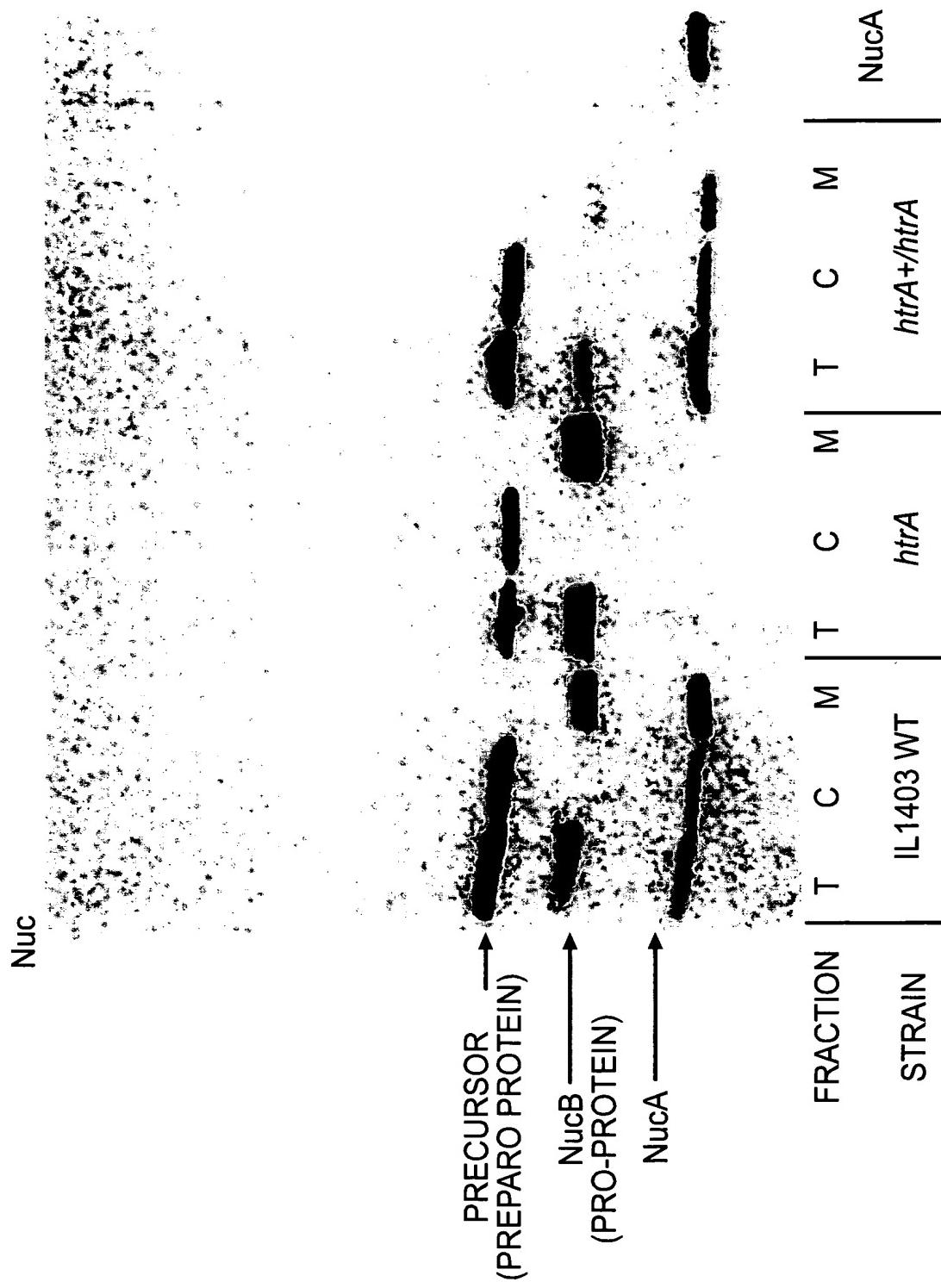


FIG. 3

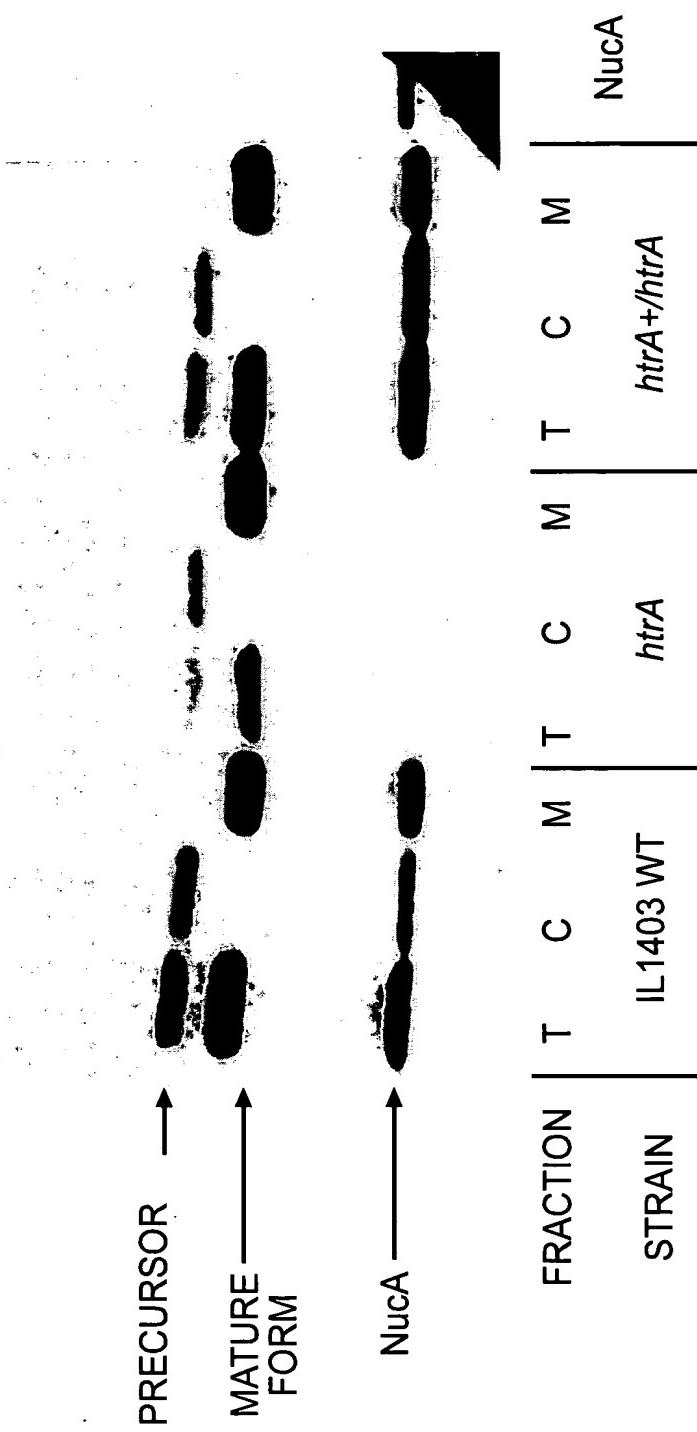
Usp- Δ SPNuc

FIG. 4

Nlp4- Δ SPNuc

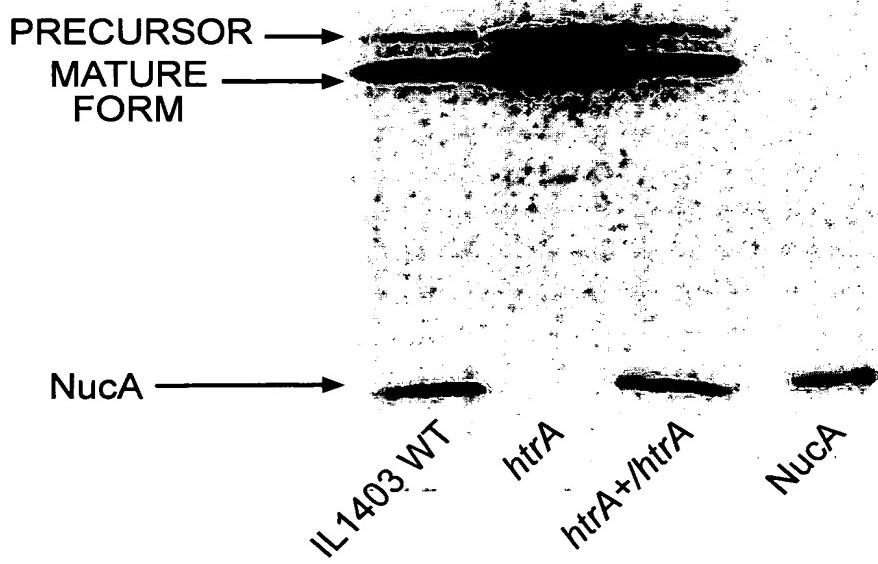


FIG. 5

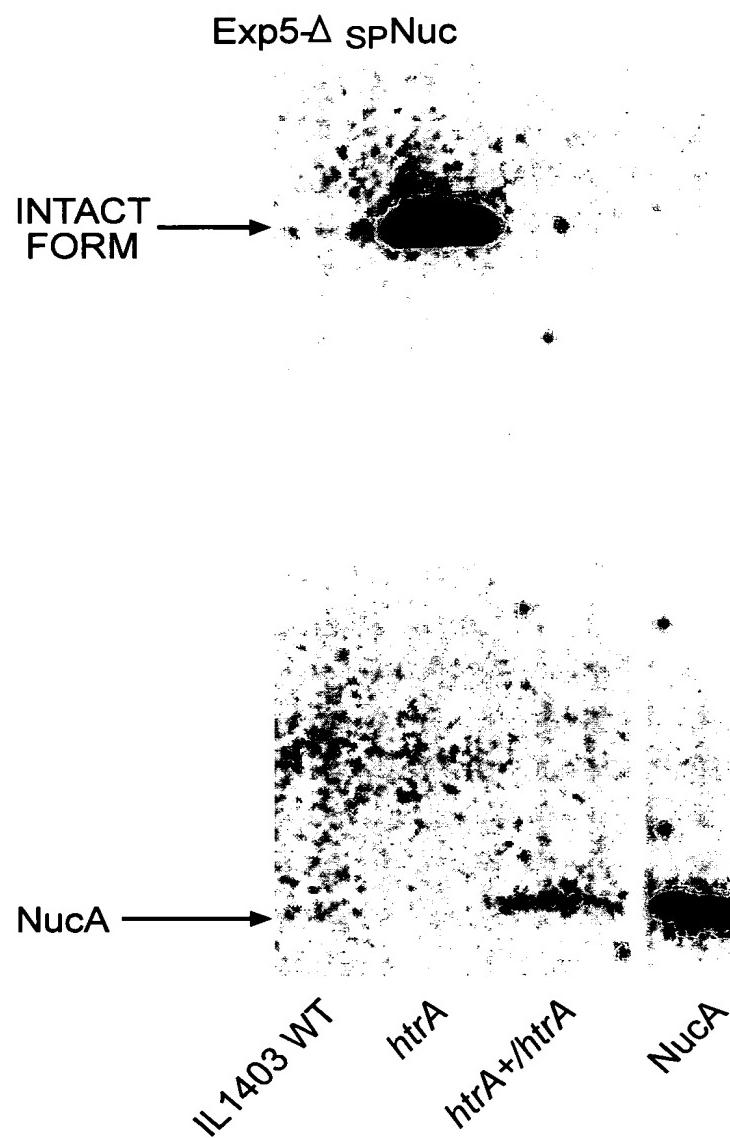


FIG. 6

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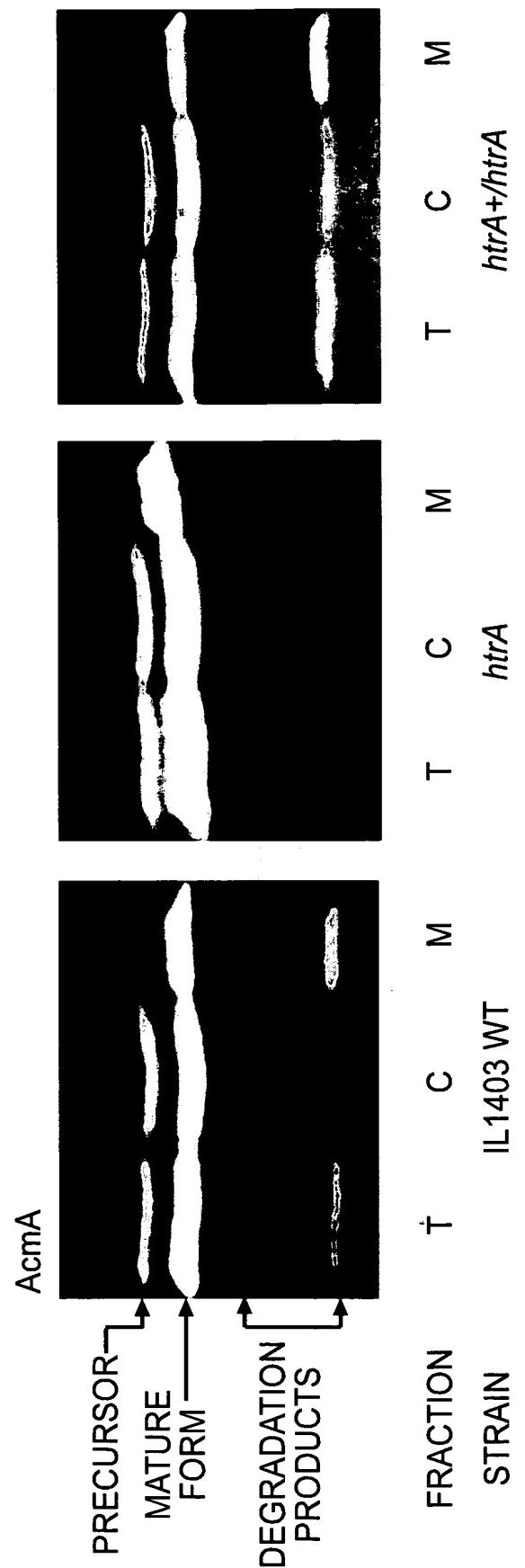


FIG. 7

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